— POSTER —

Multivariate Restricted Maximum Likelihood Estimation of Genetic Parameters for Diameter at 3 to 5 years in the *Eucalyptus globulus* Base Population in Australia

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Abstract

Genetic parameters for diameter growth at three to five years in Victoria (four sites), Tasmania (five sites), South Australia (one sites) and Western Australia (four sites) were estimated for the *Eucalyptus globulus* Labill. ssp. *globulus* base population using a derivative-free restricted maximum likelihood (DFREML) procedure applied to a multitrait individual tree model with diameter in each state used as a different trait. Within state heritabilities ranged between 0.19 and 0.27. Genetic correlations between diameter growth in different states were always above 0.62 suggesting a reduced genotype-environment interaction.

Introduction

Correct estimates of genetic and phenotypic parameters for traits of importance are needed prior to any genetic evaluation program. Traditionally, analysis of (co) variance (ANOVA) type methods have been used, but they require balanced data. Restricted maximum likelihood (REML; Patterson and Thompson 1971) has been shown to be the method of choice for estimating variance components in selected or unselected populations with unbalanced distribution of fixed effects across the classes. The aim of this study was to evaluate using an individual tree REML analysis, the genetic control of 3-5 year-old diameter growth in the *Eucalyptus globulus* ssp *globulus* base population, across a range of sites in Victoria, South Australia, Western Australia and Tasmania.

Material and Methods

The 589 open pollinated families used in this study are part of a range wide collection made in 1987 and 1988 by the CSIRO Tree Seed Centre. The families were collected across most of the range of the *E. globulus* species, and include typical populations of *Eucalyptus globulus* ssp *globulus* and populations taxonomically intermediate between this subspecies and mainland subspecies (Jordan *et al.*, 1993). The data set includes a total of 14 trials (four in Victoria, established by APM, one in South Australia established by Primary Industries S.A. (Forestry), four in Western Australia established by Bunnings Treefarms and five in Tasmania established by North Forest). Site conditions were variable but generally characterized by low altitude, low to moderately high rainfall and moderate fertility. All sites were disked and ploughed before trees were planted. Fertilizer was applied to each seedling at planting in all trials. Experimental layout was an incomplete block design with between 20 and 25 families per block in Tasmania and Western Australia and randomized complete blocks in Victoria and South Australia (see Jarvis *et al.*, 1995). Families were represented by a one to five-tree plot per block, with each family represented by up to 20 trees at each site.

Table 1. Means and number of records in the dataset.

	VIC	SA	WA	TAS
No Records	12543	3113	14182	22334
No Trees[1]	12763	3281	14552	22897
No Parents	220	168	370	563
Site.Rep. Blk	4	4	452	625
Diam Mean[2]	11.02	13.14	12.37	9.55
s.d.	2.83	2.58	3.38	3.08

[1] In the analysis, *i.e.* including parents without records. [2] After transformation.

Table 2. Estimates of variances, heritability assuming half-sib structure (*h2*), adjusted heritability (h^2_{OP}) and proportion variance due to plot effects (*c2*) for diameter at 3 to 5 years in the *Eucalyptus globulus* base population in Victoria (VIC), South Australia (SA), Western Australia (WA) and Tasmania (TAS).

Region	Variance Components					
	σ^2_A	σ^2_{plot}	σ^2_E	$h^2 \pm s.e.$	$c^2 \pm s.e$	h^2_{OP}
VIC	2.820	[1]	3.753	0.43±0.04	[1]	0.27
SA	2.797	0.208	3.362	0.44±0.07	0.03±0.01	0.27
WA	1.837	0.233	4.051	0.30±0.03	0.03±0.01	0.19
TAS	2.280	0.356	3.491	0.37±0.03	0.06±0.01	0.23

[1]Not estimated in Victoria since trials had single tree plots

Diameter at breast height (1.3m) over bark at three to five years was assessed on all surviving trees but those with any apparent disease, damage to the stem or crown or with more than one stem were removed from the analysis. Open pollinated seedlots were classified into four stand types based on descriptions and *in situ* photos taken by seed collectors, as described in Borralho and Potts (1995). For each site raw data was standardized by the ratio of the pooled phenotypic standard deviation divided by the site phenotypic standard deviation to account for differences in additive variance between sites (Visscher *et al.*, 1993).

Estimates of variance and covariance were obtained by REML using a derivative-free algorithm and fitting an individual tree model. The model used for the analysis (in matrix notation) was:

$$y = \mathbf{X}b + \mathbf{W}p + \mathbf{Z}a + e$$

where y is the vector of observations for diameter in each region, b is the vector of fixed effects, including the incomplete blocks within site, and stand type (as defined by Borralho and Potts 1995), *a* is the vector of additive genetic values of trees, *p* is the vector of random plot effects, *e* is the vector of residuals and **X**, **W** and **Z** are incidence matrices relating observations to the effects in the model. Analysis of covariance were performed considering only two traits at a time and removing plot effects from the model, in order to reduce computational requirements. In the analysis of covariances between diameter growth in two regions, the traits were measured on different trees, so residual covariances were zero (Schaeffer *et al.*, 1987). In individual tree models, information on genetic covariances is available only through relatives (half-sibs in our case) with records for the other trait. Approximate asymptotic standard errors for univariate genetic parameters were obtained from the approximate Hessian matrix (Nelder and Mean 1965). Calculations were carried out using the DFREML set of programs (Meyer 1991).

Results and discussion

Estimates of variance for transformed diameter across the four states in Australia (Victoria, South Australia, Western Australia and Tasmania) are given in Table 2. Additive genetic variance was similar across the four states, with σ^2_A between 1.84 and 2.82. Plot variance was small accounting between 3 and 6% of the total variance. Heritabilities adjusted for an open-pollinated family structure (with $r=1/2.5$) ranged between 0.19 and 0.27. These values agree well with reported estimates for growth in Portugal (Borralho *et al.*, 1992) and Australia (Volker *et al.*, 1990).

Genetic and phenotypic correlations between diameter growth at different states are presented in Table 3. It is apparent that genetic correlations are consistently high between states, with r_G ranging between 0.62 (South Australia and Western Australia) and 0.85 (Victoria and Tasmania). These values suggest that genotype-environment interactions for early growth are likely to be unimportant in Australia, a result which confirms previous studies at the provenance level (Volker and Orme 1988; Kube *et al.*, 1993). The genetic parameters reported here are being incorporated in the national BLUP genetic evaluation of *Eucalyptus globulus* (see Jarvis *et al.*, 1995).

Table 3. Genetic (above diagonal) and phenotypic correlations (below diagonal) for growth in *Eucalyptus globulus* across four plantation states.

	VIC	SA	WA	TAS
VIC		0.78	0.80	0.85
SA	0.36		0.62	0.73
WA	0.30	0.24		0.77
TAS	0.35	0.32	0.27	

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